

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/520,322  
Source: PUF  
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# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 02/02/2006

PATENT APPLICATION: US/10/520,322

TIME: 12:53:44

Input Set : A:\55382-23 SEQ LIST.txt

Output Set: N:\CRF4\02022006\J520322.raw

3 <110> APPLICANT: Katze, Michael  
 4 Bumgarner, Roger  
 5 Smit, Mariya  
 6 Rosenberg, Gary  
 8 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING HEPATOCELLULAR  
 CARCINOMA

10 <130> FILE REFERENCE: 55382-23  
 12 <140> CURRENT APPLICATION NUMBER: US 10/520,322  
 13 <141> CURRENT FILING DATE: 2004-12-30  
 15 <150> PRIOR APPLICATION NUMBER: PCT/US03/20841  
 16 <151> PRIOR FILING DATE: 2003-07-03  
 18 <150> PRIOR APPLICATION NUMBER: US60/393,982  
 19 <151> PRIOR FILING DATE: 2002-07-03  
 21 <160> NUMBER OF SEQ ID NOS: 16  
 23 <170> SOFTWARE: PatentIn version 3.3  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 195  
 27 <212> TYPE: PRT  
 28 <213> ORGANISM: Homo sapiens  
 30 <400> SEQUENCE: 1  
 32 Met Lys Leu Ala Ser Gly Phe Leu Val Leu Trp Leu Ser Leu Gly Gly  
 33 1 5 10 15  
 36 Gly Leu Ala Gln Ser Asp Thr Ser Pro Asp Thr Glu Glu Ser Tyr Ser  
 37 20 25 30  
 40 Asp Trp Gly Leu Arg His Leu Arg Gly Ser Phe Glu Ser Val Asn Ser  
 41 35 40 45  
 44 Tyr Phe Asp Ser Phe Leu Glu Leu Leu Gly Gly Lys Asn Gly Val Cys  
 45 50 55 60  
 48 Gln Tyr Arg Cys Arg Tyr Gly Lys Ala Pro Met Pro Arg Pro Gly Tyr  
 49 65 70 75 80  
 52 Lys Pro Gln Glu Pro Asn Gly Cys Gly Ser Tyr Phe Leu Gly Leu Lys  
 53 85 90 95  
 56 Val Pro Glu Ser Met Asp Leu Gly Ile Pro Ala Met Thr Lys Cys Cys  
 57 100 105 110  
 60 Asn Gln Leu Asp Val Cys Tyr Asp Thr Cys Gly Ala Asn Lys Tyr Arg  
 61 115 120 125  
 64 Cys Asp Ala Lys Phe Arg Trp Cys Leu His Ser Ile Cys Ser Asp Leu  
 65 130 135 140  
 68 Lys Arg Ser Leu Gly Phe Val Ser Lys Val Glu Ala Ala Cys Asp Ser  
 69 145 150 155 160  
 72 Leu Val Asp Thr Val Phe Asn Thr Val Trp Thr Leu Gly Cys Arg Pro  
 73 165 170 175  
 76 Phe Met Asn Ser Gln Arg Ala Ala Cys Ile Cys Ala Glu Glu Glu Lys  
 77 180 185 190

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80 Glu Glu Leu
81      195
84 <210> SEQ ID NO: 2
85 <211> LENGTH: 194
86 <212> TYPE: PRT
87 <213> ORGANISM: Homo sapiens
89 <400> SEQUENCE: 2
91 Met Lys Leu Ala Ser Gly Phe Leu Val Leu Trp Leu Ser Leu Gly Gly
92 1      5      10      15
95 Gly Leu Ala Gln Ser Asp Thr Ser Pro Asp Thr Glu Glu Ser Tyr Ser
96      20      25      30
99 Asp Trp Gly Leu Arg His Leu Arg Gly Ser Phe Glu Ser Val Asn Ser
100     35      40      45
103 Tyr Phe Asp Ser Phe Leu Glu Leu Leu Gly Gly Lys Asn Gly Val Cys
104     50      55      60
107 Gln Tyr Arg Cys Arg Tyr Gly Lys Ala Pro Met Pro Arg Pro Gly Tyr
108 65      70      75      80
111 Lys Pro Gln Glu Pro Asn Gly Cys Gly Ser Tyr Phe Leu Gly Leu Lys
112      85      90      95
115 Val Pro Glu Ser Met Asp Leu Gly Ile Pro Ala Met Thr Lys Cys Cys
116     100     105     110
119 Asn Gln Leu Asp Val Cys Tyr Asp Thr Cys Gly Ala Asn Lys Tyr Arg
120     115     120     125
123 Cys Asp Ala Lys Phe Arg Trp Cys Leu His Ser Ile Cys Ser Asp Leu
124     130     135     140
127 Lys Arg Ser Leu Gly Phe Val Ser Lys Val Glu Ala Cys Asp Ser Leu
128 145     150     155     160
131 Val Asp Thr Val Phe Asn Thr Val Trp Thr Leu Gly Cys Arg Pro Phe
132     165     170     175
135 Met Asn Ser Gln Arg Ala Ala Cys Ile Cys Ala Glu Glu Glu Lys Glu
136     180     185     190
139 Glu Leu
143 <210> SEQ ID NO: 3
144 <211> LENGTH: 464
145 <212> TYPE: PRT
146 <213> ORGANISM: Homo sapiens
148 <400> SEQUENCE: 3
150 Met Tyr Ser Asn Val Ile Gly Thr Val Thr Ser Gly Lys Arg Lys Val
151 1      5      10      15
154 Tyr Leu Leu Ser Leu Leu Leu Ile Gly Phe Trp Asp Cys Val Thr Cys
155     20      25      30
158 His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
159     35      40      45
162 Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
163     50      55      60
166 Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
167 65      70      75      80
170 Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
171     85      90      95

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174 His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
175      100      105      110
178 Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
179      115      120      125
182 Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
183      130      135      140
186 Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
187 145      150      155      160
190 Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
191      165      170      175
194 Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
195      180      185      190
198 Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
199      195      200      205
202 Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
203      210      215      220
206 Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
207 225      230      235      240
210 Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
211      245      250      255
214 Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
215      260      265      270
218 Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
219      275      280      285
222 Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
223      290      295      300
226 Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
227 305      310      315      320
230 Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
231      325      330      335
234 Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
235      340      345      350
238 Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
239      355      360      365
242 Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
243      370      375      380
246 Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
247 385      390      395      400
250 His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
251      405      410      415
254 Ser Thr Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg Val
255      420      425      430
258 Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
259      435      440      445
262 Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
263      450      455      460
266 <210> SEQ ID NO: 4
267 <211> LENGTH: 2463
268 <212> TYPE: PRT

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269 <213> ORGANISM: Homo sapiens
271 <400> SEQUENCE: 4
273 His Ile Asn Ile Asp Gln Phe Val Arg Lys Tyr Arg Ala Ala Leu Gly
274 1 5 10 15
277 Lys Leu Pro Gln Gln Ala Asn Asp Tyr Leu Asn Ser Phe Asn Trp Glu
278 20 25 30
281 Arg Gln Val Ser His Ala Lys Glu Lys Leu Thr Ala Leu Thr Lys Lys
282 35 40 45
285 Tyr Arg Ile Thr Glu Asn Asp Ile Gln Ile Ala Leu Asp Asp Ala Lys
286 50 55 60
289 Ile Asn Phe Asn Glu Lys Leu Ser Gln Leu Gln Thr Tyr Met Ile Gln
290 65 70 75 80
293 Phe Asp Gln Tyr Ile Lys Asp Ser Tyr Asp Leu His Asp Leu Lys Ile
294 85 90 95
297 Ala Ile Ala Asn Ile Ile Asp Glu Ile Ile Glu Lys Leu Lys Ser Leu
298 100 105 110
301 Asp Glu His Tyr His Ile Arg Val Asn Leu Val Lys Thr Ile His Asp
302 115 120 125
305 Leu His Leu Phe Ile Glu Asn Ile Asp Phe Asn Lys Ser Gly Ser Ser
306 130 135 140
309 Thr Ala Ser Trp Ile Gln Asn Val Asp Thr Lys Tyr Gln Ile Arg Ile
310 145 150 155 160
313 Gln Ile Gln Glu Lys Leu Gln Gln Leu Lys Arg His Ile Gln Asn Ile
314 165 170 175
317 Asp Ile Gln His Leu Ala Gly Lys Leu Lys Gln His Ile Glu Ala Ile
318 180 185 190
321 Asp Val Arg Val Leu Leu Asp Gln Leu Gly Thr Thr Ile Ser Phe Glu
322 195 200 205
325 Arg Ile Asn Asp Val Leu Glu His Val Lys His Phe Val Ile Asn Leu
326 210 215 220
329 Ile Gly Asp Phe Glu Val Ala Glu Lys Ile Asn Ala Phe Arg Ala Lys
330 225 230 235 240
333 Val His Glu Leu Ile Glu Arg Tyr Glu Val Asp Gln Gln Ile Gln Val
334 245 250 255
337 Leu Met Asp Lys Leu Val Glu Leu Thr His Gln Tyr Lys Leu Lys Glu
338 260 265 270
341 Thr Ile Gln Lys Leu Ser Asn Val Leu Gln Gln Val Lys Ile Lys Asp
342 275 280 285
345 Tyr Phe Glu Lys Leu Val Gly Phe Ile Asp Asp Ala Val Lys Lys Leu
346 290 295 300
349 Asn Glu Leu Ser Phe Lys Thr Phe Ile Glu Asp Val Asn Lys Phe Leu
350 305 310 315 320
353 Asp Met Leu Ile Lys Lys Leu Lys Ser Phe Asp Tyr His Gln Phe Val
354 325 330 335
357 Asp Glu Thr Asn Asp Lys Ile Arg Glu Val Thr Gln Arg Leu Asn Gly
358 340 345 350
361 Glu Ile Gln Ala Leu Glu Leu Pro Gln Lys Ala Glu Ala Leu Lys Leu
362 355 360 365
365 Phe Leu Glu Glu Thr Lys Ala Thr Val Ala Val Tyr Leu Glu Ser Leu

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```

366      370      375      380
369 Gln Asp Thr Lys Ile Thr Leu Ile Ile Asn Trp Leu Gln Glu Ala Leu
370 385      390      395      400
373 Ser Ser Ala Ser Leu Ala His Met Lys Ala Lys Phe Arg Glu Thr Leu
374      405      410      415
377 Glu Asp Thr Arg Asp Arg Met Tyr Gln Met Asp Ile Gln Gln Glu Leu
378      420      425      430
381 Gln Arg Tyr Leu Ser Leu Val Gly Gln Val Tyr Ser Thr Leu Val Thr
382      435      440      445
385 Tyr Ile Ser Asp Trp Trp Thr Leu Ala Ala Lys Asn Leu Thr Asp Phe
386      450      455      460
389 Ala Glu Gln Tyr Ser Ile Gln Asp Trp Ala Lys Arg Met Lys Ala Leu
390 465      470      475      480
393 Val Glu Gln Gly Phe Thr Val Pro Glu Ile Lys Thr Ile Leu Gly Thr
394      485      490      495
397 Met Pro Ala Phe Glu Val Ser Leu Gln Ala Leu Gln Lys Ala Thr Phe
398      500      505      510
401 Gln Thr Pro Asp Phe Ile Val Pro Leu Thr Asp Leu Arg Ile Pro Ser
402      515      520      525
405 Val Gln Ile Asn Phe Lys Asp Leu Lys Asn Ile Lys Ile Pro Ser Arg
406      530      535      540
409 Phe Ser Thr Pro Glu Phe Thr Ile Leu Asn Thr Phe His Ile Pro Ser
410 545      550      555      560
413 Phe Thr Ile Asp Phe Val Glu Met Lys Val Lys Ile Ile Arg Thr Ile
414      565      570      575
417 Asp Gln Met Gln Asn Ser Glu Leu Gln Trp Pro Val Pro Asp Ile Tyr
418      580      585      590
421 Leu Arg Asp Leu Lys Val Glu Asp Ile Pro Leu Ala Arg Ile Thr Leu
422      595      600      605
425 Pro Asp Phe Arg Leu Pro Glu Ile Ala Ile Pro Glu Phe Ile Ile Pro
426      610      615      620
429 Thr Leu Asn Leu Asn Asp Phe Gln Val Pro Asp Leu His Ile Pro Glu
430 625      630      635      640
433 Phe Gln Leu Pro His Ile Ser His Thr Ile Glu Val Pro Thr Phe Gly
434      645      650      655
437 Lys Leu Tyr Ser Ile Leu Lys Ile Gln Ser Pro Leu Phe Thr Leu Asp
438      660      665      670
441 Ala Asn Ala Asp Ile Gly Asn Gly Thr Thr Ser Ala Asn Glu Ala Gly
442      675      680      685
445 Ile Ala Ala Ser Ile Thr Ala Lys Gly Glu Ser Lys Leu Glu Val Leu
446      690      695      700
449 Asn Phe Asp Phe Gln Ala Asn Ala Gln Leu Ser Asn Pro Lys Ile Asn
450 705      710      715      720
453 Pro Leu Ala Leu Lys Glu Ser Val Lys Phe Ser Ser Lys Tyr Leu Arg
454      725      730      735
457 Thr Glu His Gly Ser Glu Met Leu Phe Gly Asn Ala Ile Glu Gly
458      740      745      750
461 Lys Ser Asn Thr Val Ala Ser Leu His Thr Glu Lys Asn Thr Leu Glu
462      755      760      765

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**VERIFICATION SUMMARY**

**PATENT APPLICATION: US/10/520,322**

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**Input Set : A:\55382-23 SEQ LIST.txt**

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